

Amendments to the Specification

Please replace the paragraph on lines 25-31 on page 3 with the following amended paragraph:

Rabbit and human HPRG are very similar in composition and function. Optimal alignment of the two proteins showed 63.5% sequence identity and 68.6% homology (Borza D-B. *et al.*, *Biochemistry*, 1996, 35:1925-1934). The highest homology is at the N- and C-termini. However, the apparent lower homology in the His-Pro rich domain is due to substitutions of Pro for His in the rabbit molecule. The human protein contains 15 repeats of the sequence HHPHG (SEQ ID NO:8) while the rabbit protein has 2 repeats of this sequence, 6 repeats of HPPHG (SEQ ID NO:9) and 7 repeats of PPPHG (SEQ ID NO:10). Thus a consensus sequence for these repeating units is designated [H/P][H/P]PHG (SEQ ID NO:7).

Please replace the paragraph on lines 8-20 on page 15 with the following amended paragraph:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* 48:444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available on the Worldwide web at the URL <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available on the Worldwide web at the URL <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.